RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/582,413
Source: IFWP
Date Processed by STIC: 06/22/2006

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IFWP

RAW SEQUENCE LISTING DATE: 06/22/2006
PATENT APPLICATION: **US/10/582,413** TIME: 12:52:10

Input Set : **A:\14875-164US1.txt**
Output Set: **N:\CRF4\06222006\J582413.raw**

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      3 <110> APPLICANT: Ohtomo, Toshihiko
      4       Yabuta, Naohiro
      5       Tsunoda, Hiroyuki
      6       Tsuchiya, Masayuki
      8 <120> TITLE OF INVENTION: Methods for enhancing antibody activity
     10 <130> FILE REFERENCE: 14875-164US1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/582,413
C--> 12 <141> CURRENT FILING DATE: 2006-06-09
     12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/018493
     13 <151> PRIOR FILING DATE: 2004-12-10
     15 <150> PRIOR APPLICATION NUMBER: JP 2003-415760
     16 <151> PRIOR FILING DATE: 2003-12-12
     18 <160> NUMBER OF SEQ ID NOS: 28
     20 <170> SOFTWARE: PatentIn version 3.1
     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 1924
     24 <212> TYPE: DNA
     25 <213> ORGANISM: Macaca fascicularis
     27 <220> FEATURE:
     28 <221> NAME/KEY: CDS
     29 <222> LOCATION: (11)..(1918)
     30 <223> OTHER INFORMATION:
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     34            Met Pro Ser Trp Ala Leu Phe Met Val Thr Ser Cys Leu
     35            1               5                   10
     37 ctc ctg gcc cct caa aac ctg gcc caa gtc agc agc caa gat gtc tcc        97
     38 Leu Leu Ala Pro Gln Asn Leu Ala Gln Val Ser Ser Gln Asp Val Ser
     39     15                  20                  25
     41 ttg ctg gcc tcg gac tca gag ccc ctg aag tgt ttc tcc cga aca ttt       145
     42 Leu Leu Ala Ser Asp Ser Glu Pro Leu Lys Cys Phe Ser Arg Thr Phe
     43 30                  35                  40                  45
     45 gag gac ctc act tgc ttc tgg gat gag gaa gag gca gca ccc agt ggg       193
     46 Glu Asp Leu Thr Cys Phe Trp Asp Glu Glu Glu Ala Ala Pro Ser Gly
     47                  50                  55                  60
     49 aca tac cag ctg ctg tat gcc tac ccg ggg gag aag ccc cgt gcc tgc       241
     50 Thr Tyr Gln Leu Leu Tyr Ala Tyr Pro Gly Glu Lys Pro Arg Ala Cys
     51             65                  70                  75
     53 ccc ctg agt tct cag agc gtg ccc cgc ttt gga acc cga tac gtg tgc       289
     54 Pro Leu Ser Ser Gln Ser Val Pro Arg Phe Gly Thr Arg Tyr Val Cys
     55         80                  85                  90
     57 cag ttt cca gcc cag gaa gaa gtg cgt ctc ttc tct ccg ctg cac ctc       337
     58 Gln Phe Pro Ala Gln Glu Glu Val Arg Leu Phe Ser Pro Leu His Leu
```

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59      95                  100                 105
61 tgg gtg aag aat gtg ttc cta aac cag act cag att cag cga gtc ctc      385
62 Trp Val Lys Asn Val Phe Leu Asn Gln Thr Gln Ile Gln Arg Val Leu
63 110                 115                 120                 125
65 ttt gtg gac agt gta ggc ctg ccg gct ccc ccc agt atc atc aag gcc      433
66 Phe Val Asp Ser Val Gly Leu Pro Ala Pro Pro Ser Ile Ile Lys Ala
67                 130                 135                 140
69 atg ggt ggg agc cag cca ggg gaa ctt cag atc agc tgg gag gcc cca      481
70 Met Gly Gly Ser Gln Pro Gly Glu Leu Gln Ile Ser Trp Glu Ala Pro
71             145                 150                 155
73 gct cca gaa atc agt gat ttc ctg agg tac gaa ctc cgc tat ggc ccc      529
74 Ala Pro Glu Ile Ser Asp Phe Leu Arg Tyr Glu Leu Arg Tyr Gly Pro
75         160                 165                 170
77 aaa gat ctc aag aac tcc act ggt ccc acg gtc ata cag ttg atc gcc      577
78 Lys Asp Leu Lys Asn Ser Thr Gly Pro Thr Val Ile Gln Leu Ile Ala
79     175                 180                 185
81 aca gaa acc tgc tgc cct gct ctg cag agg cca cac tca gcc tct gct      625
82 Thr Glu Thr Cys Cys Pro Ala Leu Gln Arg Pro His Ser Ala Ser Ala
83 190                 195                 200                 205
85 ctg gac cag tct cca tgt gct cag ccc aca atg ccc tgg caa gat gga      673
86 Leu Asp Gln Ser Pro Cys Ala Gln Pro Thr Met Pro Trp Gln Asp Gly
87                 210                 215                 220
89 cca aag cag acc tcc cca act aga gaa gct tca gct ctg aca gca gtg      721
90 Pro Lys Gln Thr Ser Pro Thr Arg Glu Ala Ser Ala Leu Thr Ala Val
91             225                 230                 235
93 ggt gga agc tgc ctc atc tca gga ctc cag cct ggc aac tcc tac tgg      769
94 Gly Gly Ser Cys Leu Ile Ser Gly Leu Gln Pro Gly Asn Ser Tyr Trp
95         240                 245                 250
97 ctg cag ctg cgc agc gaa cct gat ggg atc tcc ctc ggt ggc tcc tgg      817
98 Leu Gln Leu Arg Ser Glu Pro Asp Gly Ile Ser Leu Gly Gly Ser Trp
99     255                 260                 265
101 gga tcc tgg tcc ctc cct gtg act gtg gac ctg cct gga gat gca gtg      865
102 Gly Ser Trp Ser Leu Pro Val Thr Val Asp Leu Pro Gly Asp Ala Val
103 270                 275                 280                 285
105 gca att gga ctg caa tgc ttt acc ttg gac ctg aag aat gtt acc tgt      913
106 Ala Ile Gly Leu Gln Cys Phe Thr Leu Asp Leu Lys Asn Val Thr Cys
107                 290                 295                 300
109 caa tgg cag caa gag gac cat gct agt tcc caa ggt ttc ttc tac cac      961
110 Gln Trp Gln Gln Glu Asp His Ala Ser Ser Gln Gly Phe Phe Tyr His
111             305                 310                 315
113 agc agg gca cgg tgc tgc ccc aga gac agg tac ccc atc tgg gag gac     1009
114 Ser Arg Ala Arg Cys Cys Pro Arg Asp Arg Tyr Pro Ile Trp Glu Asp
115         320                 325                 330
117 tgt gaa gag gaa gag aaa aca aat cca gga tta cag acc cca cag ttc     1057
118 Cys Glu Glu Glu Glu Lys Thr Asn Pro Gly Leu Gln Thr Pro Gln Phe
119     335                 340                 345
121 tct cgc tgc cac ttc aag tca cga aat gac agc gtt att cac atc ctt     1105
122 Ser Arg Cys His Phe Lys Ser Arg Asn Asp Ser Val Ile His Ile Leu
123 350                 355                 360                 365
```

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```
125 gtg gag gtg acc aca gcc ctg ggt gct gtt cac agt tac ctg ggc tcc     1153
126 Val Glu Val Thr Thr Ala Leu Gly Ala Val His Ser Tyr Leu Gly Ser
127                 370                 375                 380
129 cct ttc tgg atc cac cag gct gtg cgc ctc ccc acc cca aac ttg cac     1201
130 Pro Phe Trp Ile His Gln Ala Val Arg Leu Pro Thr Pro Asn Leu His
131             385                 390                 395
133 tgg agg gag atc tcc agc ggg cat ctg gaa ttg gag tgg cag cac cca     1249
134 Trp Arg Glu Ile Ser Ser Gly His Leu Glu Leu Glu Trp Gln His Pro
135         400                 405                 410
137 tca tcc tgg gca gcc caa gag acc tgc tat caa ctc cga tac aca gga     1297
138 Ser Ser Trp Ala Ala Gln Glu Thr Cys Tyr Gln Leu Arg Tyr Thr Gly
139     415                 420                 425
141 gaa ggc cat cag gac tgg aag gtg ctg gag ccg cct ctc ggg gcc cga     1345
142 Glu Gly His Gln Asp Trp Lys Val Leu Glu Pro Pro Leu Gly Ala Arg
143 430                 435                 440                 445
145 gga ggg acc ctg gag ctg cgc ccg cga tct cgc tac cgt tta cag ctg     1393
146 Gly Gly Thr Leu Glu Leu Arg Pro Arg Ser Arg Tyr Arg Leu Gln Leu
147                 450                 455                 460
149 cgc gcc agg ctc aat ggc ccc acc tac caa ggt ccc tgg agc tcg tgg     1441
150 Arg Ala Arg Leu Asn Gly Pro Thr Tyr Gln Gly Pro Trp Ser Ser Trp
151             465                 470                 475
153 tcg gac cca gct agg gtg gag acc gcc acc gag acc gcc tgg att tcc     1489
154 Ser Asp Pro Ala Arg Val Glu Thr Ala Thr Glu Thr Ala Trp Ile Ser
155         480                 485                 490
157 ttg gtg acc gct ctg ctg cta gtg ctg ggc ctc agc gcc gtc ctg ggc     1537
158 Leu Val Thr Ala Leu Leu Leu Val Leu Gly Leu Ser Ala Val Leu Gly
159     495                 500                 505
161 ctg ctg ctg ctg agg tgg cag ttt cct gca cac tac agg aga ctg agg     1585
162 Leu Leu Leu Leu Arg Trp Gln Phe Pro Ala His Tyr Arg Arg Leu Arg
163 510                 515                 520                 525
165 cat gcc ctg tgg ccc tca ctt cca gat ctg cac cga gtc cta ggc cag     1633
166 His Ala Leu Trp Pro Ser Leu Pro Asp Leu His Arg Val Leu Gly Gln
167                 530                 535                 540
169 tac ctt agg gac act gca gcc ctg agt ccg ccc aag gcc aca gtc tca     1681
170 Tyr Leu Arg Asp Thr Ala Ala Leu Ser Pro Pro Lys Ala Thr Val Ser
171             545                 550                 555
173 gat acc tgt gaa gaa gtg gaa ccc agc ctc ctt gaa atc ctc ccc aag     1729
174 Asp Thr Cys Glu Glu Val Glu Pro Ser Leu Leu Glu Ile Leu Pro Lys
175         560                 565                 570
177 tcc tca gag agg act cct ttg ccc ctg tgt tcc tcc cag tcc cag atg     1777
178 Ser Ser Glu Arg Thr Pro Leu Pro Leu Cys Ser Ser Gln Ser Gln Met
179     575                 580                 585
181 gac tac cga aga ttg cag cct tct tgc ctg ggg acc atg ccc ctg tct     1825
182 Asp Tyr Arg Arg Leu Gln Pro Ser Cys Leu Gly Thr Met Pro Leu Ser
183 590                 595                 600                 605
185 gtg tgc cca ccc atg gct gag tca ggg tcc tgc tgt acc acc cac att     1873
186 Val Cys Pro Pro Met Ala Glu Ser Gly Ser Cys Cys Thr Thr His Ile
187                 610                 615                 620
189 gcc aac cat tcc tac cta cca cta agc tat tgg cag cag cct tga         1918
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```
190 Ala Asn His Ser Tyr Leu Pro Leu Ser Tyr Trp Gln Gln Pro
191             625                 630                 635
193 gtcgac                                                                1924
195 <210> SEQ ID NO: 2
196 <211> LENGTH: 635
197 <212> TYPE: PRT
198 <213> ORGANISM: Macaca fascicularis
200 <400> SEQUENCE: 2
201 Met Pro Ser Trp Ala Leu Phe Met Val Thr Ser Cys Leu Leu Leu Ala
202 1               5                  10                  15
204 Pro Gln Asn Leu Ala Gln Val Ser Ser Gln Asp Val Ser Leu Leu Ala
205             20                  25                  30
207 Ser Asp Ser Glu Pro Leu Lys Cys Phe Ser Arg Thr Phe Glu Asp Leu
208         35                  40                  45
210 Thr Cys Phe Trp Asp Glu Glu Glu Ala Ala Pro Ser Gly Thr Tyr Gln
211     50                  55                  60
213 Leu Leu Tyr Ala Tyr Pro Gly Glu Lys Pro Arg Ala Cys Pro Leu Ser
214 65                  70                  75                  80
216 Ser Gln Ser Val Pro Arg Phe Gly Thr Arg Tyr Val Cys Gln Phe Pro
217                 85                  90                  95
219 Ala Gln Glu Glu Val Arg Leu Phe Ser Pro Leu His Leu Trp Val Lys
220             100                 105                 110
222 Asn Val Phe Leu Asn Gln Thr Gln Ile Gln Arg Val Leu Phe Val Asp
223         115                 120                 125
225 Ser Val Gly Leu Pro Ala Pro Pro Ser Ile Ile Lys Ala Met Gly Gly
226     130                 135                 140
228 Ser Gln Pro Gly Glu Leu Gln Ile Ser Trp Glu Ala Pro Ala Pro Glu
229 145                 150                 155                 160
231 Ile Ser Asp Phe Leu Arg Tyr Glu Leu Arg Tyr Gly Pro Lys Asp Leu
232                 165                 170                 175
234 Lys Asn Ser Thr Gly Pro Thr Val Ile Gln Leu Ile Ala Thr Glu Thr
235             180                 185                 190
237 Cys Cys Pro Ala Leu Gln Arg Pro His Ser Ala Ser Ala Leu Asp Gln
238         195                 200                 205
240 Ser Pro Cys Ala Gln Pro Thr Met Pro Trp Gln Asp Gly Pro Lys Gln
241     210                 215                 220
243 Thr Ser Pro Thr Arg Glu Ala Ser Ala Leu Thr Ala Val Gly Gly Ser
244 225                 230                 235                 240
246 Cys Leu Ile Ser Gly Leu Gln Pro Gly Asn Ser Tyr Trp Leu Gln Leu
247                 245                 250                 255
249 Arg Ser Glu Pro Asp Gly Ile Ser Leu Gly Gly Ser Trp Gly Ser Trp
250             260                 265                 270
252 Ser Leu Pro Val Thr Val Asp Leu Pro Gly Asp Ala Val Ala Ile Gly
253         275                 280                 285
255 Leu Gln Cys Phe Thr Leu Asp Leu Lys Asn Val Thr Cys Gln Trp Gln
256     290                 295                 300
258 Gln Glu Asp His Ala Ser Ser Gln Gly Phe Phe Tyr His Ser Arg Ala
259 305                 310                 315                 320
261 Arg Cys Cys Pro Arg Asp Arg Tyr Pro Ile Trp Glu Asp Cys Glu Glu
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Output Set: N:\CRF4\06222006\J582413.raw

```
262                 325                 330                 335
264 Glu Glu Lys Thr Asn Pro Gly Leu Gln Thr Pro Gln Phe Ser Arg Cys
265             340                 345                 350
267 His Phe Lys Ser Arg Asn Asp Ser Val Ile His Ile Leu Val Glu Val
268         355                 360                 365
270 Thr Thr Ala Leu Gly Ala Val His Ser Tyr Leu Gly Ser Pro Phe Trp
271     370                 375                 380
273 Ile His Gln Ala Val Arg Leu Pro Thr Pro Asn Leu His Trp Arg Glu
274 385                 390                 395                 400
276 Ile Ser Ser Gly His Leu Glu Leu Glu Trp Gln His Pro Ser Ser Trp
277                 405                 410                 415
279 Ala Ala Gln Glu Thr Cys Tyr Gln Leu Arg Tyr Thr Gly Glu Gly His
280             420                 425                 430
282 Gln Asp Trp Lys Val Leu Glu Pro Pro Leu Gly Ala Arg Gly Gly Thr
283         435                 440                 445
285 Leu Glu Leu Arg Pro Arg Ser Arg Tyr Arg Leu Gln Leu Arg Ala Arg
286     450                 455                 460
288 Leu Asn Gly Pro Thr Tyr Gln Gly Pro Trp Ser Ser Trp Ser Asp Pro
289 465                 470                 475                 480
291 Ala Arg Val Glu Thr Ala Thr Glu Thr Ala Trp Ile Ser Leu Val Thr
292                 485                 490                 495
294 Ala Leu Leu Leu Val Leu Gly Leu Ser Ala Val Leu Gly Leu Leu Leu
295             500                 505                 510
297 Leu Arg Trp Gln Phe Pro Ala His Tyr Arg Arg Leu Arg His Ala Leu
298         515                 520                 525
300 Trp Pro Ser Leu Pro Asp Leu His Arg Val Leu Gly Gln Tyr Leu Arg
301     530                 535                 540
303 Asp Thr Ala Ala Leu Ser Pro Pro Lys Ala Thr Val Ser Asp Thr Cys
304 545                 550                 555                 560
306 Glu Glu Val Glu Pro Ser Leu Leu Glu Ile Leu Pro Lys Ser Ser Glu
307                 565                 570                 575
309 Arg Thr Pro Leu Pro Leu Cys Ser Ser Gln Ser Gln Met Asp Tyr Arg
310             580                 585                 590
312 Arg Leu Gln Pro Ser Cys Leu Gly Thr Met Pro Leu Ser Val Cys Pro
313         595                 600                 605
315 Pro Met Ala Glu Ser Gly Ser Cys Cys Thr Thr His Ile Ala Asn His
316     610                 615                 620
318 Ser Tyr Leu Pro Leu Ser Tyr Trp Gln Gln Pro
319 625                 630                 635
321 <210> SEQ ID NO: 3
322 <211> LENGTH: 24
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial
326 <220> FEATURE:
327 <223> OTHER INFORMATION: an artificially synthesized sequence
329 <400> SEQUENCE: 3
330 caggggccag tggatagact gatg                                        24
332 <210> SEQ ID NO: 4
333 <211> LENGTH: 23
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/22/2006
PATENT APPLICATION: **US/10/582,413** TIME: 12:52:11

Input Set : **A:\14875-164US1.txt**
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,9,10,11,12,13,14,15,16,17,18

VERIFICATION SUMMARY DATE: 06/22/2006
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Input Set : **A:\14875-164US1.txt**
Output Set: **N:\CRF4\06222006\J582413.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:353 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:351
L:433 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:431